

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 4, 2005, 17:11:06 ; Search time 1431 Seconds

(without alignments)
9973.393 Million cell updates/sec

Title: US-09-868-677-5

Perfect score: 2067 1 agcttcgcaccttcgacccct.....tgattcgaccccttagatttt 2067

Sequence: 1 agcttcgcaccttcgacccct.....tgattcgaccccttagatttt 2067

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 7442561 seqs, 3452328358 residues

Total number of hits satisfying chosen parameters: 14885122

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications NA.*
1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq.*
2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq.*
3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq.*
4: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq.*
5: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq.*
6: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq.*
7: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq.*
8: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq.*
9: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq.*
10: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq.*
11: /cgn2_6/ptodata/2/pubpna/US09D_PUBCOMB.seq.*
12: /cgn2_6/ptodata/2/pubpna/US09E_PUBCOMB.seq.*
13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq.*
14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq.*
15: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq.*
16: /cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq.*
17: /cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq.*
18: /cgn2_6/ptodata/2/pubpna/US10F_PUBCOMB.seq.*
19: /cgn2_6/ptodata/2/pubpna/US10G_PUBCOMB.seq.*
20: /cgn2_6/ptodata/2/pubpna/US10H_PUBCOMB.seq.*
21: /cgn2_6/ptodata/2/pubpna/US10I_PUBCOMB.seq.*
22: /cgn2_6/ptodata/2/pubpna/US10J_PUBCOMB.seq.*
23: /cgn2_6/ptodata/2/pubpna/US11A_PUBCOMB.seq.*
24: /cgn2_6/ptodata/2/pubpna/US11B_PUBCOMB.seq.*
25: /cgn2_6/ptodata/2/pubpna/US11C_PUBCOMB.seq.*
26: /cgn2_6/ptodata/2/pubpna/US11D_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match Length	ID	Description
1	813.8	39.4	1380 17	US-10-385-802-17
2	813.4	39.4	1377 17	US-10-385-802-7
3	813.4	39.4	1377 17	US-10-385-802-9
4	812.6	39.3	1389 17	US-10-385-802-31
5	812.6	39.3	1470 17	US-10-385-802-29
6	812.6	39.3	1470 17	US-10-385-802-27
7	812.6	39.3	1947 17	US-10-385-802-23

8	812.6	39.3	1998 17	US-10-385-802-25	Sequence 25, Appl
9	812.6	39.3	2094 17	US-10-385-802-47	Sequence 47, Appl
10	812.6	39.3	2118 17	US-10-385-802-21	Sequence 21, Appl
11	812.6	39.3	2181 17	US-10-385-802-19	Sequence 19, Appl
12	812.6	39.3	2652 17	US-10-385-802-1	Sequence 1, Appl
13	812.2	39.3	1377 17	US-10-385-802-11	Sequence 11, Appl
14	792.8	38.4	1589 17	US-10-385-802-45	Sequence 45, Appl
15	711.8	34.4	2003 20	US-10-385-802-43	Sequence 43, Appl
16	706.2	34.2	2003 20	US-10-809-790-3	Sequence 3, Appl
17	705.4	34.1	1359 10	US-09-773-877A-15	Sequence 15, Appl
18	705.4	34.1	1359 22	US-10-988-243-5	Sequence 5, Appl
19	705.4	34.1	1359 24	US-11-016-097-5	Sequence 5, Appl
20	705.4	34.1	1389 22	US-09-773-877A-17	Sequence 17, Appl
21	705.4	34.1	1389 22	US-10-988-243-7	Sequence 7, Appl
22	705.4	34.1	1389 24	US-11-016-097-7	Sequence 7, Appl
23	705.4	34.1	1674 10	US-09-773-877A-13	Sequence 13, Appl
24	705.4	34.1	1674 22	US-10-988-243-3	Sequence 3, Appl
25	705.4	34.1	1674 24	US-11-016-097-3	Sequence 3, Appl
26	705.4	34.1	1704 10	US-09-773-877A-11	Sequence 11, Appl
27	705.4	34.1	1704 10	US-09-773-877A-19	Sequence 19, Appl
28	705.4	34.1	1704 22	US-10-988-243-1	Sequence 1, Appl
29	705.4	34.1	1704 22	US-10-988-243-9	Sequence 9, Appl
30	705.4	34.1	1704 24	US-11-016-097-1	Sequence 1, Appl
31	705.4	34.1	1704 24	US-11-016-097-9	Sequence 9, Appl
32	705	34.1	1419 21	US-10-887-230-33	Sequence 33, Appl
33	705	34.1	1479 21	US-10-887-230-25	Sequence 25, Appl
34	702.2	34.0	2196 9	US-09-825-012-44	Sequence 44, Appl
35	702.2	34.0	2196 9	US-09-825-012-45	Sequence 45, Appl
36	702.2	34.0	2226 9	US-09-825-012-53	Sequence 53, Appl
37	702.2	34.0	2226 9	US-09-825-012-54	Sequence 54, Appl
38	700.2	33.9	1366 17	US-10-418-836-36	Sequence 36, Appl
39	700.2	33.9	1366 24	US-11-007-886-36	Sequence 36, Appl
40	700.2	33.9	1375 17	US-10-418-836-37	Sequence 37, Appl
41	700.2	33.9	1375 24	US-11-007-886-37	Sequence 37, Appl
42	700	33.9	7427 19	US-10-617-619-13	Sequence 13, Appl
43	699.4	33.8	7493 19	US-10-617-619-10	Sequence 10, Appl
44	699.4	33.8	4661 9	US-09-897-006-10	Sequence 10, Appl
45	699.4	33.8	4661 10	US-09-897-511A-10	Sequence 10, Appl

ALIGNMENTS

RESULT 1
US-10-385-802-17
Sequence 17, Application US/10385802
GENERAL INFORMATION:
APPLICANT: Dhanabai, Mohanraj
APPLICANT: Lichenstein, William J.
APPLICANT: Lichenstein, Henri
TITLE OF INVENTION: NUCLEOTIDE SEQUENCES AND AMINO ACID SEQUENCES OF
FILE REFERENCE: 15966-517UB
CURRENT APPLICATION NUMBER: US/10/385,802
PRIOR FILING DATE: 2003-03-11
PRIOR APPLICATION NUMBER: 60/363,266
PRIOR FILING DATE: 2002-03-11
NUMBER OF SEQ ID NOS: 77
SOFTWARE: Cursesqlist version 0.1
SEQ ID NO 17
LENGTH: 1380
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(1377)
US-10-385-802-17
Query Match 39.4% Score 813.8; DB 17; Length 1380;
Best Local Similarity 76.8%; Pred. No. 2.7e-219;
Matches 1040; Conservative 0; Mismatches 297; Indels 18; Gaps 3;

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 4, 2005, 17:12:22 ; Search time 169 Seconds
(without alignments)
1689.940 Million cell updates/sec

Title: US-09-868-677-6

Perfect score: 3814

Sequence: 1 MSALLILVGAIVARDCAD.....YFKGFSYSLSRTTMMIRPLD 688

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1846076 seqs, 415116000 residues

Total number of hits satisfying chosen parameters: 1846076

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
13: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*
14: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*
15: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*
16: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*
17: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*
18: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
19: /cgn2_6/ptodata/2/pubpaa/US11_PUBCOMB.pep:*
20: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
21: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2507.5	65.7	702	US-11-035-599-52	Sequence 52, Appl
2	2496.5	65.5	730	US-11-035-599-30	Sequence 30, Appl
3	2116.5	55.5	702	US-11-035-599-53	Sequence 53, Appl
4	2105.5	55.2	730	US-11-035-599-31	Sequence 31, Appl
5	1757	46.1	462	US-10-385-802-46	Sequence 46, Appl
6	1757	46.1	697	US-10-385-802-48	Sequence 48, Appl
7	1745	45.8	459	US-10-385-802-12	Sequence 12, Appl
8	1743.5	45.7	489	US-10-385-802-44	Sequence 44, Appl
9	1742	45.7	459	US-10-385-802-8	Sequence 8, Appl
10	1742	45.7	459	US-10-385-802-18	Sequence 18, Appl
11	1737	45.5	458	US-10-385-802-10	Sequence 10, Appl

12	1725.5	45.2	526	US-10-385-802-52	Sequence 52, Appl
13	1720.5	45.1	462	US-10-385-802-32	Sequence 32, Appl
14	1720.5	45.1	489	US-10-385-802-10	Sequence 10, Appl
15	1720.5	45.1	588	US-10-385-802-28	Sequence 28, Appl
16	1720.5	45.1	648	US-10-385-802-24	Sequence 24, Appl
17	1720.5	45.1	665	US-10-385-802-26	Sequence 26, Appl
18	1720.5	45.1	705	US-10-385-802-22	Sequence 22, Appl
19	1720.5	45.1	726	US-10-385-802-20	Sequence 20, Appl
20	1720.5	45.1	883	US-10-385-802-2	Sequence 2, Appl
21	1694	44.4	588	US-10-385-802-40	Sequence 40, Appl
22	1689	44.3	588	US-10-385-802-42	Sequence 42, Appl
23	1684	44.2	588	US-10-385-802-58	Sequence 58, Appl
24	1664	43.6	648	US-10-385-802-16	Sequence 16, Appl
25	1655.5	43.4	665	US-10-385-802-18	Sequence 18, Appl
26	1635.5	42.9	705	US-10-385-802-34	Sequence 34, Appl
27	1631	42.6	465	US-10-887-230-43	Sequence 43, Appl
28	1311	34.4	485	US-10-887-230-26	Sequence 26, Appl
29	1297.5	34.0	631	US-10-120-1988-2	Sequence 2, Appl
30	1295.5	34.0	659	US-10-809-790-4	Sequence 4, Appl
31	1295.5	34.0	734	US-11-035-599-50	Sequence 50, Appl
32	1295.5	34.0	949	US-10-232-838-19	Sequence 19, Appl
33	1294	33.9	641	US-10-723-003-46	Sequence 46, Appl
34	1292	33.9	452	US-09-773-877A-16	Sequence 16, Appl
35	1292	33.9	452	US-10-988-243-6	Sequence 6, Appl
36	1292	33.9	452	US-11-016-097-6	Sequence 6, Appl
37	1292	33.9	557	US-09-773-877A-14	Sequence 14, Appl
38	1292	33.9	557	US-10-988-243-4	Sequence 4, Appl
39	1292	33.9	557	US-11-016-097-4	Sequence 4, Appl
40	1292	33.9	761	US-11-035-599-29	Sequence 29, Appl
41	1292	33.9	762	US-11-035-599-28	Sequence 28, Appl
42	1291.5	33.9	731	US-11-035-599-51	Sequence 51, Appl
43	1290.5	33.8	462	US-09-773-877A-18	Sequence 18, Appl
44	1290.5	33.8	462	US-10-988-243-8	Sequence 8, Appl
45	1290.5	33.8	462	US-11-016-097-8	Sequence 8, Appl

ALIGNMENTS

RESULT 1
US-11-035-599-52
Sequence 52, Application US/11035599
Publication No. US20050158829A1
GENERAL INFORMATION:
APPLICANT: Fandl, James
APPLICANT: Chen, Gang
APPLICANT: Papadopoulos, Nicholas
APPLICANT: Aldrich, Thomas P.
TITLE OF INVENTION: Fusion Polypeptides Capable of
FILE REFERENCE: 1080A
CURRENT APPLICATION NUMBER: US/11/035, 599
CURRENT FILING DATE: 2005-01-14
PRIOR APPLICATION NUMBER: 60/536, 968
PRIOR FILING DATE: 2004-01-16
NUMBER OF SEQ ID NOS: 53
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 52
LENGTH: 702
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic
US-11-035-599-52

Query Match 65.7%, Score 2507.5, DB 20, Length 702;
Best Local Similarity 85.2%, Pred. No. 1.6e-178;
Matches 471, Conservative 14, Mismatches 27, Indels 41, Gaps 7;
QY 145 GKSSLLIHGADFTKXDNDNCMKCALMTGCGWPFADCPSPNLNGMFYAGONG-KL 203
DB 181 GKSPQLLVYGA---TNLADG-----VPSRPSGS--GSGTQYSLKI 215

OM nucleic - nucleic search, using sw model

Run on: October 4, 2005, 17:11:06 ; Search time 359 Seconds
(without alignments)
9421.125 Million cell updates/sec

Title: US-09-868-677-5
Perfect score: 2067
Sequence: 1 atgcctgaccttcgacccct.....tgattcgaccttcgacccctt 2067

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA:
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PTCTS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	705.4	34.1	1359	US-09-773-877B-15	Sequence 15, Appl
2	705.4	34.1	1389	US-09-773-877B-17	Sequence 17, Appl
3	705.4	34.1	1674	US-09-773-877B-13	Sequence 13, Appl
4	705.4	34.1	1704	US-09-773-877B-11	Sequence 11, Appl
5	705.4	34.1	1704	US-09-773-877B-19	Sequence 19, Appl
6	698.6	33.8	9209	US-08-149-099C-3	Sequence 3, Appl
7	698.6	33.8	9209	US-08-476-275-2	Sequence 2, Appl
8	698.6	33.8	9209	US-08-478-967A-3	Sequence 3, Appl
9	698.6	33.8	9209	US-08-475-815B-3	Sequence 3, Appl
10	698.6	33.8	9209	US-08-475-815-2	Sequence 2, Appl
11	698.6	33.8	18986	US-08-819-866-2	Sequence 2, Appl
12	698.6	33.8	18986	US-09-023-715-2	Sequence 2, Appl
13	698.6	33.8	18986	US-09-343-485A-2	Sequence 2, Appl
14	698.6	33.8	19040	US-09-343-485A-3	Sequence 3, Appl
15	697.4	33.7	1019	US-09-178-869-1	Sequence 1, Appl
16	697.4	33.7	1019	US-09-761-413-1	Sequence 1, Appl
17	697.4	33.7	1182	US-09-180-100-14	Sequence 14, Appl
18	697.4	33.7	1080	US-09-180-100-18	Sequence 18, Appl
19	697.4	33.7	1272	US-09-030-175-6	Sequence 6, Appl
20	697.4	33.7	1272	US-08-030-175-7	Sequence 7, Appl
21	696.8	33.7	1458	US-08-030-175-6	Sequence 6, Appl
22	696.8	33.7	1458	US-08-030-175-7	Sequence 7, Appl
23	696.8	33.7	1458	US-08-030-175-5	Sequence 5, Appl
24	696.8	33.7	1599	US-09-023-655-1120	Sequence 1120, Ap
25	696.8	33.7	1617	US-08-378-939-9	Sequence 9, Appl
26	696.6	33.7	1720	US-09-746-359A-52	Sequence 52, Appl
27	696.4	33.7	1428	US-08-488-376-19	Sequence 19, Appl

28	696.4	33.7	1428	US-08-634-223-19	Sequence 19, Appl
29	696.4	33.7	1428	US-08-634-224-19	Sequence 19, Appl
30	696.4	33.7	1428	US-08-634-400-19	Sequence 19, Appl
31	696.4	33.7	1428	US-08-635-878-19	Sequence 19, Appl
32	696.4	33.7	1428	US-08-770-057-19	Sequence 19, Appl
33	696.4	33.7	1428	US-09-335-697B-19	Sequence 19, Appl
34	696.4	33.7	1428	US-09-335-697B-19	Sequence 19, Appl
35	696.4	33.7	1428	US-09-740-002-19	Sequence 19, Appl
36	696.4	33.7	1431	US-08-487-550-3	Sequence 3, Appl
37	696.4	33.7	1431	US-08-487-550-11	Sequence 11, Appl
38	696.4	33.7	1431	US-09-526-098-3	Sequence 3, Appl
39	696.4	33.7	1431	US-09-526-098-11	Sequence 11, Appl
40	696.4	33.7	1431	US-09-383-916-3	Sequence 3, Appl
41	696.4	33.7	1431	US-09-383-916-11	Sequence 11, Appl
42	696.4	33.7	1437	US-08-487-550-7	Sequence 7, Appl
43	696.4	33.7	1437	US-09-526-098-7	Sequence 7, Appl
44	696.4	33.7	1437	US-09-383-916-7	Sequence 7, Appl
45	696.4	33.7	1494	US-09-499-846-5	Sequence 5, Appl

ALIGNMENTS

RESULT 1
US-09-773-877B-15
Sequence 15, Application US/09773877B
Patent No. 683349
GENERAL INFORMATION:
APPLICANT: Xia, Yu-Ping et al.
TITLE OF INVENTION: METHODS FOR TREATING INFLAMMATORY SKIN DISEASES
FILE REFERENCE: REG 710b
CURRENT APPLICATION NUMBER: US/09/773,877B
CURRENT FILING DATE: 2001-01-31
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn version 3.0
SEQ ID NO 15
LENGTH: 1359
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(1359)
US-09-773-877B-15

Query Match 34.1%, Score 705.4; DB 4; Length 1359;
Best Local Similarity 99.9%; Pred. No. 3.6e-184;
Matches 706; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY	691	GGCCCGGCGAGCCCAATCTTGACAAACTACACATGCCACCGTCCAGCACT	750
DB	652	GGCCCGGCGAGCCCAATCTTGACAAACTACACATGCCACCGTCCAGCACT	711
QY	751	GAACTCCCTGGGGGAGCCGTGACGCTCTTCCCTCCCAAAACCAAGGACACCTCAT	810
DB	712	GAACTCCCTGGGGGAGCCGTGACGCTCTTCCCTCCCAAAACCAAGGACACCTCAT	771
QY	811	ATCTCCCGGAGCCCTGAGTGCATCGGTGTGTGACGTGACCAAGAGACCTGAG	870
DB	772	ATCTCCCGGAGCCCTGAGTGCATCGGTGTGTGACGTGACCAAGAGACCTGAG	831
QY	871	GTCAGATTCAACTGTGACGTGACCGGTGTGACCGGTGTGACCGGTGTGACCGGT	930
DB	832	GTCAGATTCAACTGTGACGTGACCGGTGTGACCGGTGTGACCGGTGTGACCGGT	891
QY	931	GAGAGAGATGACACAGACGACGACGACGACGACGACGACGACGACGACGACGAC	990
DB	892	GAGAGAGATGACACAGACGACGACGACGACGACGACGACGACGACGACGACGAC	951
QY	991	TGGCTGATGACAGAGATCAAGTGCAGAGTCTCCAAAGAGCCCTCCAGCCCATC	1050
DB	952	TGGCTGATGACAGAGATCAAGTGCAGAGTCTCCAAAGAGCCCTCCAGCCCATC	1011

